Identifying Potential Proteasomal assembly factors and/or binding proteins using the yeast Saccharomyces cerevisiae as a model organism

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The proteasome is a large multi-protein complex responsible for the ultimate degradation of proteins in the cell. Damaged or misfolded proteins are targeted for destruction and broken down into peptides. Proteasomal degradation plays a vital role in almost every cellular process, from the cell cycle, to cell development, to apoptosis. Moreover, understanding and identifying the proteasome assembly process, important binding factors, and chaperones that assist in proteasome assembly would be pivotal in developing strategies to remedy cellular disorders caused by defects in proteasomal function. The eukaryotic proteasome is composed of two main sub-complexes, a 20S core particle and a 19S regulatory particle that caps one or both ends of the 20S core particle. The 20S core particle is the degradation component of the proteasome, and it is made up of 14 unique subunits with seven distinct α and β subunits that assemble into four stacked hetero-heptameric rings. On the β7 subunit, there is a C-terminal peptide tail that connects two halves of the 20S core particle. Previous research has shown that deletion of the β7 tail slows down proteasome assembly. We generated a yeast strain containing a deletion of the β7 tail along with deletion of two assembly factors, Pba1p and Ump1p. This strain is severely temperature sensitive and will be used to screen a plasmid-borne yeast genomic library. The goal is to potentially identify new proteasomal chaperones and/or binding partners which, when present in high copy, can overcome the defect imposed by the triple mutant.

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